

SEQUENCE LISTING

<110> Hayward, Nicholas K.
Weber, Gunther
Grimmond, Sean
Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
SAME

<130> DAVIES

<140> 08/765,588
<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 649

<212> DNA

<213> Nucleotide Sequence of VEGF165

<220>

<221> CDS

<222> (17)..(589)

<400> 1
tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt 52

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
1 5 10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100
gccc

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
15 20 25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
30 35 40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
45 50 55 60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
65 70 75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg	292		
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu			
80	90		
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cg	340		
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg			
95	100	105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag	388		
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln			
110	115	120	
·cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa	436		
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu			
125	130	135	140
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa	484		
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln			
145	150	155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc	532		
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys			
160	165	170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag	580		
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys			
175	180	185	
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg	629		
Pro Arg Arg			
190			
gaaccagatc tctcaccagg	649		

<210> 2
<211> 191
<212> PRT
<213> Nucleotide Sequence of VEGF165

```

<400> 2
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu
1           5           10          15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20          25          30

```

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45 -- -- --
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

3
a
Cont
 <210> 3
 <211> 1094
 <212> DNA
 <213> Nucleotide Sequence of SOM175

<220>
 <221> CDS
 <222> (3)...(623)
 <400> 3
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gca ctc ctg cag 47
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

cag ccc cg_g gag gt_g gt_g ccc tt_g act gt_g gag ctc at_g ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gt_g gcc aaa cag ct_g gt_g ccc agc tgc gt_g act gt_g cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ct_g gag tgt gt_g ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cg_g at_g cag atc ctc at_g atc cg_g tac cc_g agc agt cag ct_g 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110
 ggg gag at_g tcc ct_g gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gt_g aag cca gac agg gct gcc act ccc cac cac 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
 130 135 140
 cgt ccc cag ccc cgt tct gtt cc_g ggc tgg gac tct gcc ccc gga gca 479
 Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
 145 150 155
 ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
 Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
 160 165 170 175
 gcc cac gct gca ccc agc acc acc agc gcc ct_g acc ccc gga cct gcc 575
 Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
 180 185 190
 gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
 Ala Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205
 tagagctcaa cccagacacc tg_cagg_tgcc ggaagctg_cg aagg_tgacac atggctttc 683
 a³
 a³
 Cont
 aactcagca gggtgacttg cctcagaggc tatatcccag tggggaaaca aaggggagcc 743

tggtaaaaaaaaa cagccaaagcc cccaaagaccc tggcccaggc agaagctgct cttaggacctg 803
ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
tggagtaactg tctcagtttc taaccactct gtgcaagtaa gcatacttaca actggctctt 983
cctccccctca ctaagaagac ccaaacctct gcataatggg atttggcctt tggtaacaaga 1043
actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4
<211> 207
<212> PRT
<213> Nucleotide Sequence of SOM175

*α³
Cont*

<400> 4
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
130 135 140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145 150 155 160
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

165	170	175
His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro-Ala Ala		
180	185	190
Ala Ala Ala Asp Ala Ala Ser Ser Val Ala Lys Gly Gly Ala		
195	200	205
<210> 5		
<211> 993		
<212> DNA		
<213> Nuc. Seq. of SOM175 Absent Exon 6		
<220>		
<221> CDS		
<222> (3)...(566)		
<400> 5		47
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag		
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln		
1 5 10 15		
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac		95
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His		
20 25 30		
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc		143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys		
35 40 45		
cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc		191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr		
50 55 60		
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt		239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly		
65 70 75		
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac		287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His		
80 85 90 95		
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg		335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu		
100 105 110		

3
Cont.

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
 130 135 140
 cgc tgc acc cag cac cac cag cgc cct gac ccc cg^g acc tgc cgc tgc 479
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
 145 150 155
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cg^g ggc tta gag 527
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
 160 165 170 175
 ctc aac cca gac acc tgc agg tgc cg^g aag ctg cga agg tgacacatgg 576
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185
 cttttcagac tcagcagggt gacttgcc tc agaggctata tcccagtgg ggaacaaagg 636
 ggagcctggtaaaaaaacagc caagccccca agacctcagc ccaggcagaa gctgctctag 696
 gacctgggcc tctcagaggg ctcttctgcc atcccttg^c tccctgaggc catcatcaa 756
 caggacagag ttggaagagg agactggag gcagcaagag gggcacata ccagctcagg 816
 ggagaatgga gtactgtctc agtttcta^ac cactctgtgc aagtaagcat cttacaactg 876
 gctcttcctc ccctcactaa gaagacccaa acctctgcat aatgggattt gggcttggt 936
 acaagaactg tgaccccaa ccctgataaa agagatggaa ggaaaaaaaaaaaa aaaaaaaaaa 993

3
cont.

<210> 6
 <211> 188
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
 Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
 130 135 140
 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160
 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185

3
cont
 <210> 7
 <211> 858
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7
 <220>
 <221> CDS
 <222> (3)..(431)

<400> 7 47
 cc atg agc cct ctg ctc cgc cgc ctg ctg gcc gca ctc ctg cag
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cg^g gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110
 ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct a^{aa} 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
 130 135 140
 tgacacatgg ctttcagac tcagcagggt gacttgccctc agaggctata tcccagtggg 491
 ggaacaaaagg ggagcctgggt aaaaaaacagc caagccccca agacctcagc ccaggcagaa 551
 gctgctctag gacctgggcc tctcagaggg ctcttctgcc atcccttg^tc tccctgaggc 611
 catcatcaa^a caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671
 ccagctcagg ggagaatgga gtactgtctc agtttcta^ac cactctgtgc aagtaagcat 731
 cttacaactg gctttccctc ccctcactaa gaagacccaa acctctgcat aatgggattt 791
 gggctttgg^t acaagaactg tgaccccaa ccctgataaa agagatggaa ggaaaaaaaaa 851

3
 cont

aaaaaaaa

<210> 8
<211> 143
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8
Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

a³
CON.

<210> 9
<211> 910
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
<221> CDS
<222> (3)...(305)

<400> 9
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln
1 5 10 15
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag acc taaaaaaaaaag gacagtgtc tgaagccaga 335
 Gln Val Arg Met Gln Thr
 100
 cagggctgcc actccccacc accgtccccca gccccgttct gttccgggct gggactctgc 395
 ccccgagca ccctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455
 ccacgctgca cccagcacca ccagcgccct gaccccccga cctgccgctg ccgctgccga 515
 cgccgcagct tcctccgttg ccaaggcgaa ggcttagagc tcaacccaga cacctgcagg 575
 tgccggaagc tgcaagggtg acacatggct tttcagactc agcagggtga cttgcctcag 635
 aggctatatac ccagtgggaa acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggtct ttctgccatc 755
 ccttgcgtcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctggggaggca 815
 gcaagagggg tcacatacca gtcagggaa gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct cttcc

910

<210> 10
<211> 101
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10
Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Thr
100

<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaaa cg

42

a3
cont
<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13
<211> 38
<212> DNA

<213> Oligonucleotide

<400> 13
gatcctgggg ctggagtgaaa atggatgtat tcagctgg 38

<210> 14

<211> 40

<212> DNA

<213> Oligonucleotide

<400> 14
gcgggcagag gatcctgggg ctgtctggcc tcacagcact 40

<210> 15

<211> 236

<212> DNA

<213> Human SOM175

<400> 15
atgaggggcc aggtacgtga ggtctccac aggccccctgg aaagaataact tacatctgct 60
cccatggtgt atgcagggtcc gagatgtga atacagatcc tcatgcaggt gtcaggcaac 120
ttttcaagac ctaaaagacag gtgagtcctt ctcctccgta ggctgcctcc agccccaggc 180
cccccaactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16

<211> 1242

<212> DNA

<213> mVRF

<220>

<221> CDS

<222> (166)..(789)

*a³
Cmt*
<400> 16
gcacgagctc aggccgtcgc tgccggcgctg cgttgcgcgtc cctgcgccca gggctcgaaa 60
ggggggccgcg gaggagccgc cccctgcgcgc cccgcgggggg tccccgggtc cgccgcattgg 120
ggcggtctcg gctgaccccc ccccacacccg ccgggtctagg gccccg atg agc ccc ctg 177

Met Ser Pro Leu
1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu Ala Arg Thr Gln
 5 10 15 20
 gcc cct gtg tcc cag ttt gat ggc ccc agt cac cag aag aaa gtg gtg 273
 Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln Lys Lys Val Val
 25 30 35
 cca tgg ata gac gtt tat gca cgt gcc aca tgc cag ccc agg gag gtg 321
 Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln Pro Arg Glu Val
 40 45 50
 gtg gtg cct ctg agc atg gaa ctc atg ggc aat gtg gtc aaa caa cta 369
 Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val Val Lys Gln Leu
 55 60 65
 gtg ccc agc tgt gtg act gtg cag cgc tgt ggt ggc tgc tgc cct gac 417
 Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys Cys Pro Asp
 70 75 80
 gat ggc ctg gaa tgt gtg ccc act ggg caa cac caa gtc cga atg cag 465
 Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val Arg Met Gln
 85 90 95 100
 atc ctc atg atc cag tac ccg agc agt cag ctg ggg gag atg tcc ctg 513
 Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly Glu Met Ser Leu
 105 110 115
 gga gaa cac agc caa tgt gaa tgc aga cct aaa aaa aag gag agt gct 561
 Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys Glu Ser Ala
 120 125 130
 gtg agg cca gac agg gtt gcc ata ccc cac cac cgt ccc cag ccc cgc 609
 Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg
 135 140 145
 tct gtt ccg ggc tgg gac tct acc ccg gga gca ccc tcc cca gct gac 657
 Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp
 150 155 160
 atc atc cat ccc act cca gcc cca gga tcc tct gcc cgc ctt gca ccc 705
 Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro
 165 170 175 180
 agc gcc gcc aac gcc ctg acc ccc gga cct gcc gtt gcc gct gta gac 753
 Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val Ala Val Asp

<210> 17
<211> 207
<212> PRT
<213> mVRF

```

<400> 17
Met Ser Pro Leu Leu Arg Arg Leu Leu Val Ala Leu Leu Gln Leu
      5          10          15
      1
Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
      20          25          30
      20
Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
      35          40          45
      35
Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
      50          55          60
      50
Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
      65          70          75          80
      65
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
      85          90          95
      85
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
      100         105         110
      100
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
      115         120         125
      115
Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
      130         135         140
      130

```

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
 165 170 175
 Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
 180 185 190
 Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
 195 200 205

<210> 18
 <211> 188
 <212> PRT
 <213> mVRF167

<400> 18
 Met Ser Pro Leu Leu Arg Arg Leu Leu Val Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
 20 25 30
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
 50 55 60
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro
 130 135 140
 Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160
 Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys
 180

<210> 19
 <211> 188

<212> PRT
<213> hVRF167

<400> 19
Met Ser Pro Leu Leu Arg Arg Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175
Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

*3
α
Cmt*

<210> 20
<211> 71
<212> PRT
<213> mVRF186

<400> 20
Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15
Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp Ile Ile His Pro
20 25 30
Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro Ser Ala Ala Asn
35 40 45

Ala Leu Thr Pro Gly Pro Ala Val Ala Val Asp Ala Ala Ala Ser
50 55 60

Ser Ile Ala Lys Gly Gly Ala
65 70

<210> 21
<211> 71
<212> PRT
<213> hVRF186

<400> 21
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Ala Asp Ala Ala Ala Ser
50 55 60

Ser Val Ala Lys Gly Gly Ala
65 70

<210> 22
<211> 214
<212> PRT
<213> mVEGF188

<400> 22
Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
100 105 110

Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
115 120 125

Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Lys Lys Ser Val Arg
130 135 140

Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Phe Lys
145 150 155 160

Ser Trp Ser Val His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu
165 170 175

Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp
180 185 190

Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg
195 200 205

Cys Asp Lys Pro Arg Arg
210

a3

cont

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100